STIC Search Report
Biotech-Chem Library

USPTO

STIC Database Tracking Number: 139816

TO: David Lamberston
Location: rem/2b79/2c70
Art Unit: 1636
Wednesday, December 08, 2004

Case Serial Number: 09/747385

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

O'Bryen, Barbara

From: Lambertson, David

Sent: Tuesday, December 07, 2004 12:47 PM

To: O'Bryen, Barbara

Cc: Lambertson, David

Subject: Search Request

Search Request

Examiner's Name:	David Lambertson
Examiner #:	79514
Art Unit:	1636
Room #:	Remsen 02B79
Mailbox room#:	Remsen 02C70
Phone:	(571) 272-0771
Results Format:	paper

Serial #:09/747, 385

Please Search:

Nucleic Acid databases for:

SEQ ID No: 2-4 (1224 nt, 32 nt, and 132 nt, respectively)

Including:

1. Interference Search.

Also,

Protein and Nucleic Acid databases for:

SEQ ID NO: 1 (407 aa)

Including:

1. Interference Search.

Thanks,

12/7/04

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              GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:   December  7, 2004, 22:53:52 ; Search time 102.496 Seconds
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Title:           US-09-747-385-4
Perfect score:   132
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0, Gapext 1.0

Searched:        3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters:      7390102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1		42.4	32.1	24617	17	US-10-741-601-5765	Sequence 5765, Ap
2		40.4	30.6	11976	15	US-10-311-455-567	Sequence 567, Appl
3	c	40	30.3	5586	16	US-10-240-454-52	Sequence 52, Appl
4		39.2	29.7	2000	16	US-10-260-238-2019	Sequence 2019, Ap
5	c	38.8	29.4	380	17	US-10-437-963-37068	Sequence 37068, A
6	c	37.8	28.6	2140405	13	US-10-027-632-76212	Sequence 76212, A
7		37.8	28.6	2140405	15	US-10-027-632-76212	Sequence 76212, A
8	c	36.8	27.9	6699	16	US-10-240-454-15	Sequence 15, Appl
9	c	36.8	27.9	19787	15	US-10-311-455-1424	Sequence 1424, Ap
10	c	36.6	27.7	655	18	US-10-363-345A-8903	Sequence 8903, Ap
11	c	36.6	27.7	655	18	US-10-363-345A-8904	Sequence 8904, Ap
12	c	36.6	27.7	6220	15	US-10-311-455-1273	Sequence 1273, Ap
13	c	36.6	27.7	11964	17	US-10-433-793-55	Sequence 55, Appl
14	c	36.2	27.4	6048	17	US-10-433-793-31	Sequence 31, Appl
15	c	36	27.3	2000	16	US-10-260-238-2019	Sequence 2019, Ap
16		36	27.3	17538	15	US-10-311-455-1130	Sequence 1130, Ap
17	c	36	27.3	344805	18	US-10-779-271-1	Sequence 1, Appli
18	c	35.6	27.0	56153	16	US-10-221-714A-520	Sequence 520, App
19	c	35.2	26.7	17389	15	US-10-311-455-1387	Sequence 1387, Ap
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21		34.4	26.1	5379	15	US-10-311-455-1650	Sequence 1650, Ap
22		34.4	26.1	5379	15	US-10-240-485-130	Sequence 130, App
23		34.4	26.1	8576	15	US-10-311-455-2201	Sequence 2201, Ap
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25	c	34.4	26.1	3673778	15	US-10-312-841-2	Sequence 2, Appli
26	c	34.2	25.9	12590	15	US-10-311-455-1894	Sequence 1894, Ap
27		34.2	25.9	45862	13	US-10-216-355-3	Sequence 3, Appli
28		34	25.8	7047	15	US-10-240-453-259	Sequence 259, App
29		34	25.8	10183	16	US-10-221-714A-478	Sequence 478, App
30	c	33.8	25.6	722	17	US-10-437-963-37386	Sequence 37386, A
31	c	33.8	25.6	1288	16	US-10-425-114-12969	Sequence 12969, A
32	c	33.8	25.6	9095	17	US-10-443-793-92	Sequence 92, Appl
33	c	33.8	25.6	16228	16	US-10-221-613-87	Sequence 387, App
34		33.8	25.6	36604	17	US-10-739-096-5	Sequence 5, Appli
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36		33.6	25.5	483	16	US-10-424-599-70660	Sequence 70660, A
37		33.6	25.5	559	15	US-10-029-386-11887	Sequence 11887, A
38		33.6	25.5	594	17	US-10-021-323-979	Sequence 979, App
39		33.6	25.5	139214	13	US-10-087-192-2038	Sequence 2038, Ap
40	c	33.6	25.5	141079	18	US-10-331-053-56	Sequence 56, Appl
41		33.4	25.3	501	16	US-10-240-425-864	Sequence 864, App
42	c	33.4	25.3	5507	18	US-10-473-126-344	Sequence 344, App
43	c	33.4	25.3	6308	15	US-10-311-455-1444	Sequence 1444, Ap
44		33.4	25.3	80393	18	US-10-806-038-4	Sequence 4, Appli
45	c	33.4	25.3	1691139	14	US-10-067-514-1	Sequence 1, Appli

ALIGNMENTS

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; Sequence 5765, Application US/1074160l
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5765
;   LENGTH: 24617
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5765

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  Best Local Similarity   60.3%;  Pred. No. 0.91;
  Matches   70;  Conservative   0;  Mismatches  46;  Indels   0;  Gaps   0;

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Db   19206 AGATTTACTTTATATACAGGGCAAAAGGTAAATCATACAGACCCATTTGTCAATTTA 19265

Qy      77 CAGGACAAATTTCAACTTTAACAGGACAAATTTCAACTTTAACAGGACAAATTT 132
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Db   19266 TTTTTGAATTTAAATTTAAAGGGACAAATACTTCATTTTAACAAGGTATATGT 19321

RESULT 2
US-10-311-455-567
; Sequence 567, Application US/10311455
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            GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:      December 7, 2004, 21:22:51 ; Search time 18.6792 Seconds
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Perfect score:   132
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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	3	34	25.8	1888	3	US-09-035-648-20	Sequence 20, Appl
	4	34	25.8	1888	3	US-09-001-951-20	Sequence 20, Appl
	5	34	25.8	1888	4	US-08-818-829-20	Sequence 20, Appl
	6	33.2	25.2	640681	4	US-09-790-988-1	Sequence 1, Appli
	7	32.8	24.8	6072	3	US-09-535-381-3	Sequence 3, Appli
c	8	32.2	24.4	5804	4	US-08-956-171E-249	Sequence 249, App
c	9	32.2	24.4	5804	4	US-08-781-986A-249	Sequence 249, App
c	10	32	24.2	188	3	US-08-905-124-3	Sequence 3, Appli
c	11	32	24.2	1308	3	US-09-601-198-3	Sequence 3, Appli
c	12	32	24.2	6306	4	US-10-204-708-50	Sequence 50, Appl
c	13	32	24.2	6866	4	US-10-204-708-19	Sequence 19, Appl
	14	32	24.2	7502	3	US-08-969-644-6	Sequence 6, Appli
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c	26	31	23.5	2003	3	US-09-270-767-13299	Sequence 13299, A
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	28	30.8	23.3	319608	4	US-09-539-333D-1	Sequence 1, Appli
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ALIGNMENTS

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US-08-947-823-1

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;-   APPLICANT:  Williamson, Valerie M.
;-   APPLICANT:  Kaloshian, Isgouhi
;-   APPLICANT:  Yaghoobi, Jafar
;-   APPLICANT:  Bodeau, John
;-   APPLICANT:  Milligan, Stephen
;-   TITLE OF INVENTION:  Procedures and Materials for Conferring
;-   TITLE OF INVENTION:  Pest Resistance in Plants
;-   NUMBER OF SEQUENCES:  5
;-   CORRESPONDENCE ADDRESS:
;-     ADDRESSEE:  Townsend and Townsend and Crew LLP
;-     STREET:  Two Embarcadero Center, Eighth Floor
;-     CITY:  San Francisco
;-     STATE:  California
;-     COUNTRY:  USA
;-     ZIP:  94111-3834
;-   COMPUTER READABLE FORM:
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;-     COMPUTER:  IBM PC compatible
;-     OPERATING SYSTEM:  PC-DOS/MS-DOS
;-     SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;-     FILING DATE:  09-OCT-1997
;-     CLASSIFICATION:  800
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;-     APPLICATION NUMBER:  PCT/US97/18802
;-     FILING DATE:  09-OCT-1997
;-   PRIOR APPLICATION DATA:
;-     APPLICATION NUMBER:  US 60/028,191
;-     FILING DATE:  10-OCT-1996
;-   ATTORNEY/AGENT INFORMATION:
;-     NAME:  Bastian, Kevin L.
;-     REGISTRATION NUMBER:  34,774
;-     REFERENCE/DOCKET NUMBER:  023070-070210US
;-   TELECOMMUNICATION INFORMATION:
;-     TELEPHONE:  (415) 576-0200
;-     TELEFAX:  (415) 576-0300
;- INFORMATION FOR SEQ ID NO: 1:
;-   SEQUENCE CHARACTERISTICS:
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;-     TYPE:  nucleic acid
;-     STRANDEDNESS:  single
;-     TOPOLOGY:  linear
;-     MOLECULE TYPE:  DNA (genomic)
US-08-947-823-1
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                 GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        December 7, 2004, 22:53:52 ; Search time 17.0827 Seconds
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Scoring table: IDENTITY_NUC
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Searched:      3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters:    7390102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c	5	17.4	79.1	753	16	US-10-424-599-104890	Sequence 104890,
	6	17.4	79.1	1087	13	US-10-027-632-9376	Sequence 9376, Ap
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	8	17.2	78.2	1254	16	US-10-282-122A-36263	Sequence 36263, A
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	15	17.2	78.2	626	18	US-10-425-115-99166	Sequence 99166, A
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c	17	17.2	78.2	873	13	US-10-027-632-172293	Sequence 172293,
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	30	17.2	78.2	3084	8	US-08-825-486-11	Sequence 11, Appl
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	32	17.2	78.2	3084	9	US-09-372-044-11	Sequence 11, Appl
	33	17.2	78.2	3084	10	US-09-560-150-6	Sequence 6, Appli
	34	17.2	78.2	3084	14	US-10-067-741-6	Sequence 6, Appli
c	35	17.2	78.2	7158	15	US-10-369-493-26066	Sequence 26066, A
c	36	17.2	78.2	9834	8	US-08-781-986A-37	Sequence 37, Appl
	37	17.2	78.2	9834	16	US-10-329-624-37	Sequence 37, Appl
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	39	17.2	78.2	90468	15	US-10-085-117-160	Sequence 160, App
	40	16.8	76.4	182	18	US-10-425-115-150471	Sequence 150471,
	41	16.8	76.4	476	13	US-10-027-632-45431	Sequence 45431, A
c	42	16.8	76.4	476	15	US-10-027-632-45431	Sequence 45431, A
c	43	16.8	76.4	488	13	US-10-027-632-265888	Sequence 265888,
	44	16.8	76.4	488	15	US-10-027-632-265888	Sequence 265888,
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; Sequence 6022, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
;  APPLICANT: Terry, Roemer D.
;  APPLICANT: Bo, Jiang
;  APPLICANT: Charles, Boone
;  APPLICANT: Howard, Bussey
;  TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
;  FILE REFERENCE: 10182-005-999
;  CURRENT APPLICATION NUMBER: US/10/032,585
;  CURRENT FILING DATE: 2001-12-20
;  NUMBER OF SEQ ID NOS: 8000
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 6022
;  LENGTH: 984
;  TYPE: DNA
;  ORGANISM: Candida albicans
US-10-032-585-6022

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; Sequence 3733, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
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6	17.2	78.2	3083	2	US-08-616-844-36	Sequence 36, Appl
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18	17.2	78.2	3084	3	US-09-298-292A-6	Sequence 6, Appli
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20	17.2	78.2	3084	4	US-08-825-486-11	Sequence 11, Appl
21	17.2	78.2	3084	4	US-08-826-248-11	Sequence 11, Appl
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26	16.8	76.4	1914	4	US-09-690-454-34	Sequence 34, Appl
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28	16.4	74.5	250	4	US-09-513-999C-23096	Sequence 23096, A
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38	16.2	73.6	499	4	US-09-679-409-56	Sequence 56, Appl
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; APPLICANT: Keith Weinstock et al
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; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
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; ORGANISM: Candida albicans
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; Sequence 21, Application US/09792024
; Patent No. 6783985
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; TITLE OF INVENTION: Targets Discovery
; FILE REFERENCE: 10182-004-999
; CURRENT APPLICATION NUMBER: US/09/792,024
; CURRENT FILING DATE: 2001-02-20
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
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; TYPE: DNA

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       Copyright (c) 1993 - 2004 Compugen Ltd.

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c 6	166	13.6	6292	16	US-10-221-714A-461				Sequence 461, App
c 7	162.2	13.3	3683	15	US-10-221-714A-339				Sequence 339, App
c 8	158.6	13.0	15548	18	US-10-311-455-2128				Sequence 2128, Ap
c 9	156.6	12.8	3683	18	US-10-473-126-193				Sequence 193, App
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c 11	152.8	12.5	1297	18	US-10-425-115-67687				Sequence 67687, A
c 12	152.4	12.5	15387	15	US-10-311-455-157				Sequence 157, App

c 13	151.6	12.4	8056	18	US-10-473-126-386		Sequence 386, App
c 14	151.4	12.4	1243	18	US-10-425-115-172717		Sequence 172717,
c 15	150.6	12.3	975	18	US-10-363-345A-16099		Sequence 16099, A
c 16	150.6	12.3	975	18	US-10-363-345A-16100		Sequence 16100, A
c 17	148.4	12.1	1204	17	US-10-437-963-77858		Sequence 77858, A
c 18	148.4	12.1	8056	18	US-10-473-126-386		Sequence 386, App
c 19	148	12.1	8056	18	US-10-473-126-240		Sequence 240, App
c 20	147	12.0	14006	15	US-10-311-455-1931		Sequence 1931, Ap
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c 22	145.6	11.9	1062	18	US-10-425-115-120013		Sequence 120013,
c 23	144	11.8	17967	15	US-10-311-455-988		Sequence 988, App
c 24	143.4	11.7	5413	15	US-10-311-455-537		Sequence 537, App
c 25	143.2	11.7	1004	18	US-10-425-115-81106		Sequence 81106, A
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c 28	142.6	11.6	9964	15	US-10-240-453-53		Sequence 53, Appl
c 29	142.2	11.6	1130	18	US-10-311-455-71		Sequence 71, Appl
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c 31	141	11.5	1121	18	US-10-425-115-115706		Sequence 115706,
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;  APPLICANT: Agilent Technologies
;  TITLE OF INVENTION: Methods and Systems for Nanopore Data Analysis
;  FILE REFERENCE: 50112-1580
;  CURRENT APPLICATION NUMBER: US/10/668,749A
;  CURRENT FILING DATE: 2003-09-23
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c	34	91.2	7.5	19124	2	US-08-487-826B-13	Sequence 13, Appl
	35	90.4	7.4	3680	3	US-09-647-390-15	Sequence 15, Appl
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	37	89.4	7.3	9347	4	US-10-204-708-36	Sequence 36, Appl
	38	89.2	7.3	6801	4	US-10-204-708-62	Sequence 62, Appl
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ALIGNMENTS

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; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellems, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-487-826B-13

Query Match   9.4%; Score 114.8; DB 2; Length 19124;
Best Local Similarity 49.8%; Pred. No. 9e-11;

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            Copyright (c) 1993 - 2004 Compugen Ltd.

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and is derived by analysis of the total score distribution.

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5	198.5	9.6	5528	16	US-10-415-253-1	Sequence 1, Appli
6	198.5	9.6	6152	9	US-09-742-096-1	Sequence 1, Appli
7	196	9.4	3510	15	US-10-369-493-24782	Sequence 24782, A
8	193.5	9.3	3475	10	US-09-883-343A-15	Sequence 15, Appl
9	193.5	9.3	3393	15	US-10-117-937-597	Sequence 597, App
10	192.5	9.3	3393	17	US-10-657-022-93	Sequence 93, Appl
11	191.5	9.2	2564	18	US-10-416-330-12	Sequence 12, Appl
12	190	9.1	3546	16	US-10-282-122A-17261	Sequence 17261, A
13	189	9.1	3492	16	US-10-282-122A-15680	Sequence 15680, A
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23	181.5	8.7	2643	15	US-10-369-493-45330	Sequence 45330, A
24	181.5	8.7	5641	15	US-10-032-585-6646	Sequence 6646, Ap
25	181	8.7	3588	16	US-10-282-122A-16553	Sequence 16553, A
26	181	8.7	4410	17	US-10-473-576-25	Sequence 25, Appl
27	180.5	8.7	5628	15	US-10-369-493-45972	Sequence 45972, A
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30	179.5	8.6	6386	13	US-10-098-841-40	Sequence 40, Appl
31	178	8.6	2728	16	US-10-302-172-62	Sequence 62, Appl
32	178	8.6	3471	15	US-10-369-493-23730	Sequence 23730, A
33	178	8.6	4350	17	US-10-473-576-45	Sequence 45, Appl
34	177.5	8.5	2171	18	US-10-416-330-6	Sequence 6, Appli
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; Publication No. US2003023367SA1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 24748
; LENGTH: 3018
; TYPE: DNA
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        Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 14 | 178 | 8.6 | 3763 | 1 | US-07-792-865D-1 | Sequence 1, Appli |
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| 20 | 168.5 | 8.1 | 2718 | 4 | US-09-248-796A-2230 | Sequence 2230, Ap |
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ALIGNMENTS

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; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	247	11.9	1005	14	US-10-369-493-1061	Sequence 1061, Ap
2	225	10.8	1178	15	US-10-282-122A-52434	Sequence 52434, A
3	216	10.4	1790	14	US-10-369-493-1586	Sequence 1586, Ap
4	198.5	9.6	1786	9	US-09-742-096-3	Sequence 3, Appli
5	198.5	9.6	1787	15	US-10-415-253-2	Sequence 1095, Appli
6	196	9.4	1169	14	US-10-369-493-1095	Sequence 1095, App
7	192.5	9.3	976	14	US-10-117-937-596	Sequence 596, App
8	192.5	9.3	976	16	US-10-657-022-92	Sequence 92, Appl
9	191.5	9.2	795	16	US-10-408-765A-1205	Sequence 1205, Ap
10	191.5	9.2	795	17	US-10-416-330-34	Sequence 34, Appl
11	190	9.1	1182	15	US-10-282-122A-53445	Sequence 53445, A
12	189	9.1	1163	15	US-10-282-122A-51864	Sequence 51864, A
13	188.5	9.1	950	15	US-10-282-122A-47285	Sequence 47285, A
14	187.5	9.0	1294	15	US-10-282-122A-61292	Sequence 61292, A
15	187.5	9.0	1805	10	US-09-820-843A-73	Sequence 73, Appl
16	187.5	9.0	1805	15	US-10-282-122A-63513	Sequence 63513, A
17	185.5	8.9	944	14	US-10-369-493-1682	Sequence 1682, Ap
18	183.5	8.8	759	15	US-10-335-977-8694	Sequence 8694, Ap
19	183.5	8.8	762	15	US-10-335-977-8695	Sequence 8695, Ap
20	181.5	8.7	880	14	US-10-369-493-21643	Sequence 21643, A
21	181.5	8.7	1881	15	US-10-032-585-7646	Sequence 7646, Ap
22	181	8.7	1196	15	US-10-282-122A-52737	Sequence 52737, A
23	181	8.7	1404	16	US-10-473-576-2	Sequence 2, Appli
24	180.5	8.7	1875	14	US-10-369-493-22285	Sequence 22285, A
25	180	8.7	1125	15	US-10-282-122A-47213	Sequence 47213, A
26	179.5	8.6	743	14	US-10-087-464-53	Sequence 53, Appl
27	178	8.6	1156	14	US-10-369-493-43	Sequence 43, Appl
28	178	8.6	1384	16	US-10-473-576-22	Sequence 22, Appl
29	178	8.6	1948	14	US-10-032-585-7611	Sequence 7611, Ap
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31	173	8.3	687	15	US-10-282-122A-57797	Sequence 57797, A
32	173	8.3	879	13	US-10-108-605-217	Sequence 217, App
33	172.5	8.3	891	14	US-10-369-493-13477	Sequence 13477, A
34	172	8.3	497	10	US-09-820-843A-32	Sequence 32, Appl
35	172	8.3	1191	15	US-10-282-122A-52048	Sequence 52048, A
36	171.5	8.3	1818	15	US-10-282-122A-64245	Sequence 64245, A
37	171	8.2	819	15	US-10-282-122A-47000	Sequence 47000, A
38	170.5	8.2	696	16	US-10-408-765A-1067	Sequence 1067, Ap
39	170	8.2	670	9	US-09-748-875-63	Sequence 63, Appl
40	170	8.2	670	10	US-09-298-523B-63	Sequence 63, Appl
41	170	8.2	1979	14	US-10-205-823-419	Sequence 419, App
42	169	8.1	996	9	US-09-815-242-5251	Sequence 5251, Ap
43	169	8.1	1009	9	US-09-815-242-12141	Sequence 12141, A
44	168.5	8.1	567	14	US-10-094-749-2480	Sequence 2480, Ap
45	168.5	8.1	613	17	US-10-416-330-29	Sequence 29, Appl

ALIGNMENTS

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; Sequence 1061, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1061
; LENGTH: 1005
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
US-10-369-493-1061

Query Match             11.9%;  Score 247;  DB 14;  Length 1005;
Best Local Similarity   24.4%;  Pred. No. 1.6e-05;
Matches  109;  Conservative   85;  Mismatches  165;  Indels   88;  Gaps   20;

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Wed Dec 8 09:08:20 2004

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              GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    December 7, 2004, 18:31:43 ; Search time 39 Seconds
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                              692.088 Million cell updates/sec

Title:           US-09-747-385-1
Perfect score:   2077
Sequence:        1 MDFSSIKKSLGLINFRDLKK.........ELEENIKRMQELNKLKKEV 407
Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters:     478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	198.5	9.6	1786	3	US-08-973-462-8	Sequence 8, Appli
2	197	9.5	241	4	US-09-107-532A-4086	Sequence 4086, Ap
3	192.5	9.3	976	3	US-09-104-324B-4	Sequence 4, Appli
4	192.5	9.3	976	1	US-09-538-092-1339	Sequence 1339, Ap
5	180.5	8.7	740	3	US-08-257-077-5	Sequence 5, Appli
6	175	8.4	710	4	US-09-107-532A-5067	Sequence 5067, Ap
7	172.5	8.3	1078	4	US-09-248-796A-20284	Sequence 20284, A
8	172	8.3	742	3	US-09-248-796A-19053	Sequence 19053, A
9	171.5	8.3	924	4	US-09-248-796A-18798	Sequence 18798, A
10	169.5	8.2	1211	3	US-09-134-001C-4820	Sequence 4820, Ap
11	168.5	8.1	905	4	US-09-248-796A-16333	Sequence 16333, A
12	168	8.1	1010	3	US-09-134-001C-5178	Sequence 5178, Ap
13	167	8.0	2954	4	US-09-150-867-1	Sequence 8, Appli
14	166.5	8.0	630	3	US-09-248-796A-20275	Sequence 20275, A
15	163	7.8	810	4	US-09-248-796A-20281	Sequence 20281, A
16	162	7.8	1098	4	US-09-538-092-1044	Sequence 1044, Ap
17	162	7.8	1427	3	US-08-923-992A-6	Sequence 6, Appli
18	161	7.8	1128	3	US-08-923-992A-2	Sequence 2, Appli
19	161	7.8	1164	3	US-08-750-590-2	Sequence 2, Appli
20	161	7.8	1401	1	US-08-220-958-2	Sequence 2, Appli
21	160.5	7.7	384	3	US-09-308-375-2	Sequence 2, Appli
22	160.5	7.7	2285	3	US-09-595-684B-31	Sequence 31, Appl
23	160.5	7.7	2663	4	US-09-538-092-1252	Sequence 1252, Ap
24	160	7.7	2663	3	US-09-722-139-2	Sequence 2, Appli
25	160	7.7	1375	3	US-09-721-832-2	Sequence 2, Appli
26	160	7.7	1375	3	US-09-721-689-2	Sequence 2, Appli
27	160	7.7	1375	4	US-09-721-689-2	Sequence 2, Appli
28	159.5	7.7	1354	3	US-08-685-871-2	Sequence 2, Appli
29	159.5	7.7	2482	1	US-08-328-254-6	Sequence 6, Appli
30	159.5	7.7	3210	4	US-09-538-092-1154	Sequence 1154, Ap
31	159	7.7	472	4	US-09-166-350-17	Sequence 17, Appl
32	158.5	7.6	583	4	US-09-710-279-1358	Sequence 1358, Ap
33	158.5	7.6	3248	1	US-08-353-700-1	Sequence 1, Appli
34	158.5	7.6	3248	5	PCT-US95-16216-1	Sequence 1, Appli
35	158	7.6	645	2	US-08-592-126-144	Sequence 144, App
36	158	7.6	645	2	US-08-687-080-47	Sequence 47, Appl
37	158	7.6	645	4	US-09-168-595-144	Sequence 144, App
38	158	7.6	668	4	US-09-328-352-6586	Sequence 6586, Ap
39	158	7.6	1312	2	US-08-592-126-148	Sequence 148, App
40	158	7.6	1312	2	US-08-687-080-51	Sequence 51, Appl
41	158	7.6	1312	4	US-09-168-595-148	Sequence 148, App
42	157.5	7.6	496	4	US-09-543-681A-6465	Sequence 6465, Ap
43	157	7.6	448	4	US-09-248-796A-20279	Sequence 20279, A
44	156.5	7.5	1104	3	US-08-923-992A-4	Sequence 4, Appli
45	156.5	7.5	1173	4	US-09-248-796A-19313	Sequence 19313, A

ALIGNMENTS

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RESULT 1
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; Sequence 8, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 0660-0125-0 PCT
; CURRENT APPLICATION NUMBER: US/08/973,462B
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: PCT/FR96/00894
; EARLIER FILING DATE: 1996-06-12
; EARLIER APPLICATION NUMBER: FR 95/07007
; EARLIER FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 8
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Polypeptide
US-08-973-462-8

  Query Match             9.6%;  Score 198.5;  DB 3;  Length 1786;
  Best Local Similarity   22.2%;  Pred. No. 3.6e-05;
  Matches  103;  Conservative  105;  Mismatches  172;  Indels  85;  Gaps  24;

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